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Identification and Quantification fo Bacteria in Prosthetic Joint Specimens by Molecular Methods

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Symposium of The Danish Microbiological Society, November 9th, 2010

Poster: IDENTIFICATION AND QUANTIFICATION OF BACTERIA IN PROSTHETIC JOINT SPECIMENS BY MOLECULAR METHODS

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The diagnosis of prosthetic infection remains challenging. This study compared the bacterial diversity in surgical samples from 22 prosthetic patients using standard culture methods and culture-independent molecular methods including broad range 16S rRNA gene analysis, quantitative PCR (qPCR), and fluorescence *in situ* hybridization (FISH). Molecular methods detected bacteria in samples from 12 patients. Using clone libraries 40 different species were identified including known pathogens and species not previously reported in orthopaedic infections. Polymicrobial infections were found in 9 patients. Culture-based methods showed bacterial growth in 8 cases, of which 7 were monomicrobial. Neither anaerobe nor species not previously described in implant infections was isolated. Overall, the results of culture-based and molecular methods showed concordance in 11 cases (hereof 9 negative by both methods) and discrepancy in 6 cases. In the remaining 5 cases, culture methods identified one species or a group of bacteria (*e.g.*, coryneform rods), while molecular methods detected several distinct species including the species identified by culture. QPCR was used to quantify *Propionibacterium* and *S. aureus*. These quantifications confirmed the findings from the clone library approach. Additionally, both single cells and microcolonies were visualized using FISH and confocal scanning laser microscopy.